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| National Institutes of Health, Department of Health and Human Services |

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| DNAWorks Web Site: http://helixweb.nih.gov/dnaworks |

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| Send all correspondence to webtools@helix.nih.gov |

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Job started on 09/23/2011 at 19:51:16

Job name: RS092311MptpBRv0153c

Output will be sent to ronnie-13@sbcglobal.net

SEQUENCE 1: PROTEIN LENGTH = 277

----------------------------------------------------------------

1 MAVRELPGAWNFRDVADTATALRPGRLFRSSELSRLDDAGRATLRRLGITDVADLRSSRE

61 VARRGPGRVPDGIDVHLLPFPDLADDDADDSAPHETAFKRLLTNDGSNGESGESSQSIND

121 AATRYMTDEYRQFPTRNGAQRALHRVVTLLAAGRPVLTHCFAGKDRTGFVVALVLEAVGL

181 DRDVIVADYLRSNDSVPQLRARISEMIQQRFDTELAPEVVTFTKARLSDGVLGVRAEYLA

241 AARQTIDETYGSLGGYLRDAGISQATVNRMRGVLLGX

----------------------------------------------------------------

CODON FREQUENCY TABLE: E. coli Class II

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TTT F 0.291 TCT S 0.324 TAT Y 0.352 TGT C 0.389

TTC F 0.709 TCC S 0.266 TAC Y 0.648 TGC C 0.612

TTA L 0.034 TCA S 0.048 TAA X 0.630 TGA X 0.352

TTG L 0.055 TCG S 0.074 TAG X 0.076 TGG W 1.000

CTT L 0.056 CCT P 0.112 CAT H 0.298 CGT R 0.643

CTC L 0.080 CCC P 0.016 CAC H 0.702 CGC R 0.330

CTA L 0.008 CCA P 0.153 CAA Q 0.187 CGA R 0.011

CTG L 0.767 CCG P 0.719 CAG Q 0.814 CGG R 0.008

ATT I 0.335 ACT T 0.291 AAT N 0.173 AGT S 0.045

ATC I 0.659 ACC T 0.536 AAC N 0.828 AGC S 0.243

ATA I 0.006 ACA T 0.047 AAA K 0.786 AGA R 0.006

ATG M 1.000 ACG T 0.127 AAG K 0.215 AGG R 0.003

GTT V 0.398 GCT A 0.275 GAT D 0.461 GGT G 0.508

GTC V 0.135 GCC A 0.161 GAC D 0.540 GGC G 0.428

GTA V 0.200 GCA A 0.240 GAA E 0.754 GGA G 0.020

GTG V 0.268 GCG A 0.323 GAG E 0.247 GGG G 0.044

ACTIVE CODONS FOR SEQUENCE GENERATION

Residue Codons Active Codons Min. Freq. Max. Freq.

----------------------------------------------------------------

A Ala 4 4 0.161 0.323

C Cys 2 2 0.389 0.612

D Asp 2 2 0.461 0.540

E Glu 2 2 0.247 0.754

F Phe 2 2 0.291 0.709

G Gly 4 2 0.428 0.508

H His 2 2 0.298 0.702

I Ile 3 2 0.335 0.659

K Lys 2 2 0.215 0.786

L Leu 6 2 0.080 0.767

M Met 1 1 1.000 1.000

N Asn 2 2 0.173 0.828

P Pro 4 3 0.112 0.719

Q Gln 2 2 0.187 0.814

R Arg 6 2 0.330 0.643

S Ser 6 3 0.243 0.324

T Thr 4 3 0.127 0.536

V Val 4 4 0.135 0.398

W Trp 1 1 1.000 1.000

X End 3 2 0.352 0.630

Y Tyr 2 2 0.352 0.648

SEQUENCE PATTERNS TO BE SCREENED

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PARAMETERS FOR TRIAL 1

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Total Size Of Gene ......... 831 nt

Protein Residues ........... 277

Mutatable Residues ......... 272

Fixed Nucleotides .......... 15 nt

Oligo Size ................. 60 nt

Annealing Temp ............. 62 +/- 1\*C

Oligo Concentration ........ 1.00E-7 M

Sodium Concentration ....... 5.00E-2 M

Mg2+ Concentration ......... 2.00E-3 M

Codon Frequency Threshold .. 10%

Repeat Threshold ........... 8 nt

Mispriming Threshold ....... 8/18 (6 exact) nt

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The DNA sequence # 1 is:

----------------------------------------------------------------

1 ATGGCGGTTCGTGAACTGCCGGGTGCGTGGAACTTTCGTGATGTTGCGGACACCGCGACC

61 GCGCTGCGCCCTGGTCGTCTCTTCCGTTCTTCTGAACTGTCTCGCCTGGATGATGCCGGT

121 CGTGCGACCCTCCGCCGTCTGGGTATCACCGATGTCGCGGACCTCCGCTCTTCTCGTGAA

181 GTTGCACGTCGTGGTCCAGGCCGCGTCCCGGACGGTATCGACGTTCACCTGCTGCCGTTC

241 CCGGATCTGGCTGATGACGACGCGGATGACAGCGCTCCGCATGAAACCGCGTTCAAACGT

301 CTGCTGACCAACGATGGCTCTAACGGTGAAAGCGGTGAATCTTCTCAGTCTATCAACGAC

361 GCAGCGACGCGTTACATGACCGACGAATACCGCCAATTTCCGACCCGCAACGGTGCGCAA

421 CGTGCCCTGCATCGTGTAGTTACCCTGCTCGCGGCAGGCCGTCCAGTACTCACCCACTGT

481 TTCGCGGGCAAAGACCGTACCGGTTTTGTGGTTGCGCTGGTTCTGGAAGCGGTTGGCCTC

541 GATCGTGACGTTATCGTTGCAGACTACCTGCGTTCTAATGACTCTGTTCCGCAGCTCCGT

601 GCGCGTATCTCTGAAATGATCCAGCAGCGTTTCGACACCGAACTCGCGCCTGAAGTCGTT

661 ACCTTCACCAAAGCGCGTCTGAGCGACGGCGTTCTCGGTGTACGCGCTGAATACCTGGCG

721 GCTGCGCGTCAGACCATCGACGAAACGTACGGCTCTCTGGGTGGCTACCTCCGTGACGCG

781 GGTATTTCTCAGGCGACCGTTAATCGTATGCGTGGTGTGCTCCTGGGTTAA

----------------------------------------------------------------

The oligonucleotide assembly is:

----------------------------------------------------------------

1 10 20 30 40 50 60

| | | | | | |

1 --->

1 ATGGCGGTTCGTGAACTGCCGGGTGCGTGGAACTTTCG

CCCACGCACCTTGAAAGCACTACAACGCCTGTGGCGCTGG

M A V R E L P G A W N F R D V A D T A T

| | | | | | |

3 --->

61 gcgccctggtcgtctcttccgttcttctgaactgtctcgcctggatgatgccggt

CGCGACGCGGGACCAGCAGA ctactacggcca

<--- 2

A L R P G R L F R S S E L S R L D D A G

| | | | | | |

5 --->

121 cgtgc GTCGCGGACCTCCGCTCTTCTCGTGAA

gcacgctgggaggcggcagacccatagtggctacagcgcctggaggcg

<--- 4

R A T L R R L G I T D V A D L R S S R E

| | | | | | |

181 GTTGCACGTCGTGGTCCAGGCCGCGTCCCGGAC

CGGCGCAGGGCCTGCCATAGCTGCAAGTGGACGACGGCAAG

V A R R G P G R V P D G I D V H L L P F

| | | | | | |

7 --->

241 cggatctggctgatgacgacgcggatgacagcgctccgcatgaaaccgcgttcaaacgt

GGCCTAGACCGACTACTGC ctttggcgcaagtttgca

<--- 6

P D L A D D D A D D S A P H E T A F K R

| | | | | | |

9 --->

301 c CGGTGAAAGCGGTGAATCTTCTCAGTCTATCAACGAC

gacgactggttgctaccgagattgccactttcgccacttaga

<--- 8

L L T N D G S N G E S G E S S Q S I N D

| | | | | | |

11 --->

361 GCAGCGACGCGTTACATGACCGA cggtgcgcaa

CTGCGCAATGTACTGGCTGCTTATGGCGGTTAAAGGCTGGGCGTTGCCACGCGTT

<-

A A T R Y M T D E Y R Q F P T R N G A Q

| | | | | | |

421 cgtgccctgcatcgtgtagttaccctgctcgcggcaggccgtccagtact

GCACG cgtccggcaggtcatgagtgggtgaca

-- 10

R A L H R V V T L L A A G R P V L T H C

| | | | | | |

13 --->

481 CCGTACCGGTTTTGTGGTTGCGCTGGTTCTGGAAGCGGTTGGCCTC

aagcgcccgtttctggcatggccaaaacaccaa CGGAG

<--- 12

F A G K D R T G F V V A L V L E A V G L

| | | | | | |

15 --->

541 GATCGTGACGTTAT aatgactctgttccgcagctccgt

CTAGCACTGCAATAGCAACGTCTGATGGACGCAAGATTACTGAGACAAGGCGTCG

<--- 14

D R D V I V A D Y L R S N D S V P Q L R

| | | | | | |

601 gcgcgtatctctgaaatgatccagcagcgtttcgac

taggtcgtcgcaaagctgtggcttgagcgcggacttcagcaa

A R I S E M I Q Q R F D T E L A P E V V

| | | | | | |

17 --->

661 CCTTCACCAAAGCGCGTCTGAGCGACGGCGTTCTCGGTGTACGCGCTGAATACCTGGCG

tggaagtggtttcgcgca GCGACTTATGGACCGC

<--- 16

T F T K A R L S D G V L G V R A E Y L A

| | | | | | |

19 --->

721 G gtacggctctctgggtggctacctccgtgacgcg

CGACGCGCAGTCTGGTAGCTGCTTTGCATGCCGAGAGACCCACC

<--- 18

A A R Q T I D E T Y G S L G G Y L R D A

| | | | | | |

781 ggtatttctcaggcgaccgttaatcg

gagtccgctggcaattagcatacgcaccacacgaggacccaatt

<--- 20

G I S Q A T V N R M R G V L L G X

----------------------------------------------------------------

The total codon usage score ........... 0.000

The total length score ................ 0.000

The total melting temperature score ... 0.000

The total repeat score ................ 0.000

The total pattern score ............... 0.000

The total mispriming score ............ 0.000

The total AT content score ............ 0.000

The total GC content score ............ 0.000

The total fixed gap score ............. N/A

The OVERALL score ...... 0.000

DETAILED CODON FREQUENCY REPORT

[ Codon, AA, Frequency, # of times used in coding sequence ]

----------------------------------------------------------------

TTT F 0.29 3 TCT S 0.32 14 TAT Y 0.35 0 TGT C 0.39 1

TTC F 0.71 6 TCC S 0.27 0 TAC Y 0.65 6 TGC C 0.61 0

TTA L 0.03 0 TCA S 0.05 0 TAA X 0.63 1 TGA X 0.35 0

TTG L 0.06 0 TCG S 0.07 0 TAG X 0.08 0 TGG W 1.00 1

CTT L 0.06 0 CCT P 0.11 2 CAT H 0.30 2 CGT R 0.64 25

CTC L 0.08 11 CCC P 0.02 0 CAC H 0.70 2 CGC R 0.33 8

CTA L 0.01 0 CCA P 0.15 2 CAA Q 0.19 2 CGA R 0.01 0

CTG L 0.77 19 CCG P 0.72 7 CAG Q 0.81 6 CGG R 0.01 0

ATT I 0.34 1 ACT T 0.29 0 AAT N 0.17 2 AGT S 0.05 0

ATC I 0.66 7 ACC T 0.54 16 AAC N 0.83 5 AGC S 0.24 3

ATA I 0.01 0 ACA T 0.05 0 AAA K 0.79 3 AGA R 0.01 0

ATG M 1.00 4 ACG T 0.13 2 AAG K 0.22 0 AGG R 0.00 0

GTT V 0.40 14 GCT A 0.28 4 GAT D 0.46 9 GGT G 0.51 15

GTC V 0.14 3 GCC A 0.16 2 GAC D 0.54 17 GGC G 0.43 8

GTA V 0.20 3 GCA A 0.24 4 GAA E 0.75 13 GGA G 0.02 0

GTG V 0.27 2 GCG A 0.32 22 GAG E 0.25 0 GGG G 0.04 0

Frequency Range Number of Codons

-------------------------------------

0% - 4% 0

5% - 9% 11

10% - 14% 7

15% - 19% 8

20% - 24% 10

25% - 29% 11

30% - 34% 45

35% - 39% 15

40% - 44% 8

45% - 49% 9

>= 50% 153

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Total Codons Used = 277

Tm Range # of Overlaps

-------------------------------------

<59 0

59 0

60 0

61 11

62 8

63 0

64 0

65 0

66 0

>=67 0

-------------------------------------

Tm Range = 1.7

Ovrlap Len Range # of Oligos

-------------------------------------

<14 0

14 1

15 3

16 0

17 4

18 5

19 6

20 0

21 0

22 0

23 0

>=24 0

-------------------------------------

Lowest Overlap = 14

Length Range # of Oligos

-------------------------------------

<50 2

50-51 0

52-53 0

54-55 0

56-57 0

58-59 0

60-61 18

62-63 0

64-65 0

66-67 0

68-69 0

>=70 0

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Longest = 60

Sequence Patterns Screened (As Supplied By User)

----------------------------------------------------------------

None found

----------------------------------------------------------------

20 oligonucleotides need to be synthesized

----------------------------------------------------------------

1 ATGGCGGTTCGTGAACTGCCGGGTGCGTGGAACTTTCG 38

2 AGACGACCAGGGCGCAGCGCGGTCGCGGTGTCCGCAACATCACGAAAGTTCCACGCACCC 60

3 GCGCCCTGGTCGTCTCTTCCGTTCTTCTGAACTGTCTCGCCTGGATGATGCCGGTCGTGC 60

4 GCGGAGGTCCGCGACATCGGTGATACCCAGACGGCGGAGGGTCGCACGACCGGCATCATC 60

5 GTCGCGGACCTCCGCTCTTCTCGTGAAGTTGCACGTCGTGGTCCAGGCCGCGTCCCGGAC 60

6 CGTCATCAGCCAGATCCGGGAACGGCAGCAGGTGAACGTCGATACCGTCCGGGACGCGGC 60

7 CGGATCTGGCTGATGACGACGCGGATGACAGCGCTCCGCATGAAACCGCGTTCAAACGTC 60

8 AGATTCACCGCTTTCACCGTTAGAGCCATCGTTGGTCAGCAGACGTTTGAACGCGGTTTC 60

9 CGGTGAAAGCGGTGAATCTTCTCAGTCTATCAACGACGCAGCGACGCGTTACATGACCGA 60

10 GCACGTTGCGCACCGTTGCGGGTCGGAAATTGGCGGTATTCGTCGGTCATGTAACGCGTC 60

11 CGGTGCGCAACGTGCCCTGCATCGTGTAGTTACCCTGCTCGCGGCAGGCCGTCCAGTACT 60

12 AACCACAAAACCGGTACGGTCTTTGCCCGCGAAACAGTGGGTGAGTACTGGACGGCCTGC 60

13 CCGTACCGGTTTTGTGGTTGCGCTGGTTCTGGAAGCGGTTGGCCTCGATCGTGACGTTAT 60

14 GCTGCGGAACAGAGTCATTAGAACGCAGGTAGTCTGCAACGATAACGTCACGATCGAGGC 60

15 AATGACTCTGTTCCGCAGCTCCGTGCGCGTATCTCTGAAATGATCCAGCAGCGTTTCGAC 60

16 ACGCGCTTTGGTGAAGGTAACGACTTCAGGCGCGAGTTCGGTGTCGAAACGCTGCTGGAT 60

17 CCTTCACCAAAGCGCGTCTGAGCGACGGCGTTCTCGGTGTACGCGCTGAATACCTGGCGG 60

18 CCACCCAGAGAGCCGTACGTTTCGTCGATGGTCTGACGCGCAGCCGCCAGGTATTCAGCG 60

19 GTACGGCTCTCTGGGTGGCTACCTCCGTGACGCGGGTATTTCTCAGGCGACCGTTAATCG 60

20 TTAACCCAGGAGCACACCACGCATACGATTAACGGTCGCCTGAG 44

FINAL SUMMARY FOR 1 SOLUTION

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# Tm Len | Score TmRange Short Long #Olig #Repeat #Misprime

1 62 60 | 0.000 1.7 14 60 20 0 0

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